



## SEQUENCE LISTING

## (1) GENERAL INFORMATION

(i) APPLICANT: Coleman, Roger  
Bandman, Olga  
Wilde, Craig G.

(ii) TITLE OF THE INVENTION: NEW CHEMOKINES EXPRESSED IN PANCREAS

(iii) NUMBER OF SEQUENCES: 11

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: U.S.  
(F) ZIP: 94304

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: DOS  
(D) SOFTWARE: FastSEQ Version 1.5

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER: 08/390,740  
(B) FILING DATE: February 17, 1995

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Luther, Barbara J.  
(B) REGISTRATION NUMBER: 33,954  
(C) REFERENCE/DOCKET NUMBER: PF-0027 US

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 415-855-0555  
(B) TELEFAX: 415-852-0195

## (2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 291 base pairs  
(B) TYPE: nucleic acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(vii) IMMEDIATE SOURCE:

(A) LIBRARY: Human Pancreas  
(B) CLONE: 223187

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

ATGAAGGTCT	CCGCAGCACT	TCTGTGGCTG	CTGCTCATAG	CAGCTGCCTT	CAGCCCCCAG	60
GGGCTCACTG	GGCCAGCTTC	TGTCCCAACC	ACCTGCTGCT	TTAACCTGGC	CAATAGGAAG	120
ATACCCCTTC	AGCGACTAGA	GAGCTACAGG	AGAATCACCA	GTGGCAAATG	TCCCCAGAAA	180
GCTGTGATCT	TCAAGACCAA	ACTGGCCAAG	GATATCTGTG	CCGACCCAA	GAAGAAAGTGG	240
GTGCAGGATT	CCATGAAGTA	TCTGGACCAA	AAATCTCCAA	CTCCAAAGCCA		291

## (2) INFORMATION FOR SEQ ID NO:2:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 97 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human Pancreas
- (B) CLONE: 223187

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Lys	Val	Ser	Ala	Ala	Leu	Leu	Trp	Leu	Leu	Leu	Ile	Ala	Ala	Ala
1				5					10				15		
Phe	Ser	Pro	Gln	Gly	Leu	Thr	Gly	Pro	Ala	Ser	Val	Pro	Thr	Thr	Cys
					20			25					30		
Cys	Phe	Asn	Leu	Ala	Asn	Arg	Lys	Ile	Pro	Leu	Gln	Arg	Leu	Glu	Ser
					35			40			45				
Tyr	Arg	Arg	Ile	Thr	Ser	Gly	Lys	Cys	Pro	Gln	Lys	Ala	Val	Ile	Phe
					50			55			60				
Lys	Thr	Lys	Leu	Ala	Lys	Asp	Ile	Cys	Ala	Asp	Pro	Lys	Lys	Lys	Trp
65					70				75			80			
Val	Gln	Asp	Ser	Met	Lys	Tyr	Leu	Asp	Gln	Lys	Ser	Pro	Thr	Pro	Lys
					85				90			95			
Pro															

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 402 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: cDNA

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human Pancreas
- (B) CLONE: 226152

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

ATGGCTCAGT	CACTGGCTCT	GAGCCTCCTT	ATCCTGGTTC	TGGCCTTTGG	CATCCCCAGG	60
ACCCAAGGCA	GTGATGGAGG	GGCTCAGGAC	TGTTGCCTCA	AGTACAGCCA	AAGGAAGATT	120

CCCGCCAAGG	TTGTCCGCAG	CTACCGGAAG	CAGGAACCAA	GCTTAGGCTG	CTCCATCCCA	180
GCTATCCTGT	TCTTGCCCCG	CAAGCGCTCT	CAGGCAGAGC	TATGTGCAGA	CCCAAAGGAG	240
CTCTGGGTGC	AGCAGCTGAT	GCAGCATCTG	GACAAGACAC	CATCCCCACA	GAAACCAGCC	300
CAGGGCTGCA	GGAAGGACAG	GGGGGCCTCC	AAGACTGGCA	AGAAAGGAAA	GGGCTCCAAA	360
GGCTGCAAGA	GGACTGAGCG	GTCACAGACC	CCTAAAGGGC	CA		402

## (2) INFORMATION FOR SEQ ID NO:4:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 134 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: Human Pancreas
- (B) CLONE: 226152

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

Met	Ala	Gln	Ser	Leu	Ala	Leu	Ser	Leu	Leu	Ile	Leu	Val	Leu	Ala	Phe
1				5				10					15		
Gly	Ile	Pro	Arg	Thr	Gln	Gly	Ser	Asp	Gly	Gly	Ala	Gln	Asp	Cys	Cys
					20			25					30		
Leu	Lys	Tyr	Ser	Gln	Arg	Lys	Ile	Pro	Ala	Lys	Val	Val	Arg	Ser	Tyr
					35			40				45			
Arg	Lys	Gln	Glu	Pro	Ser	Leu	Gly	Cys	Ser	Ile	Pro	Ala	Ile	Leu	Phe
					50			55			60				
Leu	Pro	Arg	Lys	Arg	Ser	Gln	Ala	Glu	Leu	Cys	Ala	Asp	Pro	Lys	Glu
					65			70		75			80		
Leu	Trp	Val	Gln	Gln	Leu	Met	Gln	His	Leu	Asp	Lys	Thr	Pro	Ser	Pro
					85			90				95			
Gln	Lys	Pro	Ala	Gln	Gly	Cys	Arg	Lys	Asp	Arg	Gly	Ala	Ser	Lys	Thr
					100			105				110			

Gly Lys Lys Gly Lys Gly Ser Lys Gly Cys Lys Arg Thr Glu Arg Ser  
     115                     120                     125  
 Gln Thr Pro Lys Gly Pro  
     130

## (2) INFORMATION FOR SEQ ID NO:5:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 97 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

Met Lys Val Ser Ala Ala Leu Leu Ala Leu Leu Leu Ile Ala Ala Ala  
     1                     5                     10                     15  
 Phe Cys Pro Gln Gly Leu Ala Gln Pro Asp Gly Val Asp Thr Pro Thr  
     20                     25                     30  
 Thr Cys Cys Phe Asn Tyr Ile Asn Arg Lys Ile Pro Arg Gln Arg Leu  
     35                     40                     45  
 Glu Ser Tyr Arg Arg Ile Thr Ser Ser Lys Cys Ser Lys Pro Ala Val  
     50                     55                     60  
 Ile Phe Lys Thr Lys Arg Ala Lys Gln Val Cys Ala Asp Pro Lys Glu  
     65                     70                     75                     80  
 Lys Trp Val Gln Asp Ser Met Lys His Leu Asp Lys Gln Thr Pro Lys  
     85                     90                     95  
 Pro

## (2) INFORMATION FOR SEQ ID NO:6:

- (i) SEQUENCE CHARACTERISTICS:
  - (A) LENGTH: 92 amino acids
  - (B) TYPE: amino acid
  - (C) STRANDEDNESS: single
  - (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vii) IMMEDIATE SOURCE:
 

- (A) LIBRARY: GenBank
- (B) CLONE: MIP-1 $\alpha$

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

Met Gln Val Ser Thr Ala Ala Leu Ala Val Leu Leu Cys Thr Met Ala  
     1                     5                     10                     15  
 Leu Cys Asn Gln Phe Ser Ala Ser Leu Ala Ala Asp Thr Pro Thr Ala  
     20                     25                     30  
 Cys Cys Phe Ser Tyr Thr Ser Arg Gln Ile Pro Gln Asn Phe Ile Ala  
     35                     40                     45  
 Asp Tyr Phe Glu Thr Ser Ser Gln Cys Ser Lys Pro Gly Val Ile Phe  
     50                     55                     60

Leu	Thr	Lys	Arg	Ser	Arg	Gln	Val	Cys	Ala	Asp	Pro	Ser	Glu	Glu	Trp
65					70				75					80	
Val	Gln	Lys	Tyr	Val	Ser	Asp	Leu	Glu	Leu	Ser	Ala				
				85					90						

## (2) INFORMATION FOR SEQ ID NO:7:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 92 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: MIP-1b

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

Met	Lys	Leu	Cys	Val	Thr	Val	Leu	Ser	Leu	Leu	Met	Leu	Val	Ala	Ala
1					5				10				15		
Phe	Cys	Ser	Pro	Ala	Leu	Ser	Ala	Pro	Met	Gly	Ser	Asp	Pro	Pro	Thr
					20				25				30		
Ala	Cys	Cys	Phe	Ser	Tyr	Thr	Ala	Arg	Lys	Leu	Pro	Arg	Asn	Phe	Val
					35				40			45			
Val	Asp	Tyr	Tyr	Glu	Thr	Ser	Ser	Leu	Cys	Ser	Gln	Pro	Ala	Val	Val
					50				55			60			
Phe	Gln	Thr	Lys	Arg	Ser	Lys	Gln	Val	Cys	Ala	Asp	Pro	Ser	Glu	Ser
65					70				75			80			
Trp	Val	Gln	Glu	Tyr	Val	Tyr	Asp	Leu	Glu	Leu	Asn				
					85				90						

## (2) INFORMATION FOR SEQ ID NO:8:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 91 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: RANTES

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Met	Lys	Val	Ser	Ala	Ala	Arg	Leu	Ala	Val	Ile	Leu	Ile	Ala	Thr	Ala
1					5				10			15			
Leu	Cys	Ala	Pro	Ala	Ser	Ala	Ser	Pro	Tyr	Ser	Ser	Asp	Thr	Thr	Pro
					20				25			30			

Cys	Cys	Phe	Ala	Tyr	Ile	Ala	Arg	Pro	Leu	Pro	Arg	Ala	His	Ile	Lys
35						40						45			
Glu	Tyr	Phe	Tyr	Thr	Ser	Gly	Lys	Cys	Ser	Asn	Pro	Ala	Val	Val	Phe
50						55						60			
Val	Thr	Arg	Lys	Asn	Arg	Gln	Val	Cys	Ala	Asn	Pro	Glu	Lys	Lys	Trp
65						70				75			80		
Val	Arg	Glu	Tyr	Ile	Asn	Ser	Leu	Glu	Met	Ser					
					85					90					

## (2) INFORMATION FOR SEQ ID NO:9:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 99 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: MCP-1

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

Met	Lys	Val	Ser	Ala	Ala	Leu	Leu	Cys	Leu	Leu	Leu	Ile	Ala	Ala	Thr
1						5			10				15		
Phe	Ile	Pro	Gln	Gly	Leu	Ala	Gln	Pro	Asp	Ala	Ile	Asn	Ala	Pro	Val
						20			25			30			
Thr	Cys	Cys	Tyr	Asn	Phe	Thr	Asn	Arg	Lys	Ile	Ser	Val	Gln	Arg	Leu
						35			40			45			
Ala	Ser	Tyr	Arg	Arg	Ile	Thr	Ser	Ser	Lys	Cys	Pro	Lys	Glu	Ala	Val
						50			55			60			
Ile	Phe	Lys	Thr	Ile	Val	Ala	Lys	Glu	Ile	Cys	Ala	Asp	Pro	Lys	Gln
						65			70			75			80

Lys Trp Val Gln Asp Ser Met Asp His Leu Asp Lys Gln Thr Gln Thr  
85 90 95  
Pro Lys Thr

## (2) INFORMATION FOR SEQ ID NO:10:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 77 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: MCP-2

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Ala Gln Pro Asp Ser Val Ser Ile Pro Ile Thr Cys Cys Phe Asn Val  
1 5 10 15  
Ile Asn Arg Lys Ile Pro Ile Gln Arg Leu Glu Ser Tyr Thr Arg Ile  
20 25 30  
Thr Asn Ile Gln Cys Pro Lys Glu Ala Val Ile Phe Lys Thr Lys Arg  
35 40 45  
Gly Lys Glu Val Cys Ala Asp Pro Lys Glu Arg Trp Val Arg Asp Ser  
50 55 60  
Met Lys His Leu Asp Gln Ile Phe Gln Asn Leu Lys Pro  
65 70 75

## (2) INFORMATION FOR SEQ ID NO:11:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 109 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (ii) MOLECULE TYPE: peptide

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GenBank
- (B) CLONE: MCP-3

## (vi) ORIGINAL SOURCE:

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

Met Trp Lys Pro Met Pro Ser Pro Ser Asn Met Lys Ala Ser Ala Ala  
1 5 10 15  
Leu Leu Cys Leu Leu Leu Thr Ala Ala Ala Phe Ser Pro Gln Gly Leu  
20 25 30  
Ala Gln Pro Val Gly Ile Asn Thr Ser Thr Thr Cys Cys Tyr Arg Phe  
35 40 45  
Ile Asn Lys Lys Ile Pro Lys Gln Arg Leu Glu Ser Tyr Arg Arg Thr  
50 55 60  
Thr Ser Ser His Cys Pro Arg Glu Ala Val Ile Phe Lys Thr Lys Leu  
65 70 75 80  
Asp Lys Glu Ile Cys Ala Asp Pro Thr Gln Lys Trp Val Gln Asp Phe  
85 90 95  
Met Lys His Leu Asp Lys Lys Thr Gln Thr Pro Lys Leu  
100 105